<110> Legos, Jeffrey F
      Barone, Frank T
      Coatney, Robert

<120> METHODS OF TREATMENT WITH LXR AGONISTS

<130> PU60406

<140> TO BE ASSIGNED
<141> 2003-07-22

<150> 60/489,202
<151> 2002-07-22

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1344
<212> DNA
<213> Homo sapien

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agagaggaag ccaggatgcc ccactctgct gggggtactg caggggtggg gctggaggct 180
gcagagccca cagccctgct caccagggca gagccccctt cagaacccac agagatccgt 240
ccacaaaagc ggaaaaaggg gccagccccc aaaatgctgg ggaacgagct atgcagcgtg 300
tgtggggaca aggcctcggg cttccactac aatgttctga gctgcgaggg ctgcaaggga 360
ttcttccgcc gcagcgtcat caagggagcg cactacatct gccacagtgg cggccactgc 420
cccatggaca cctacatgcg tcgcaagtgc caggagtgtc ggcttcgcaa atgccgtcag 480
gctggcatgc gggaggagtg tgtcctgtca gaagaacaga tccgcctgaa gaaactgaag 540
cggcaagagg aggaacaggc tcatgccaca tccttgcccc ccaggcgttc ctcacccccc 600
caaatcctgc cccagctcag cccggaacaa ctgggcatga tcgagaagct cgtcgctgcc 660
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gcaccagatc cccatagccg ggaggcccgt cagcagcgct ttgcccactt cactgagctg 780
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gctatcagca tcttctctgc agaccggccc aacgtgcagg accagctcca ggtgggagag 1140
ctgcagcaca catatgtgga agccctgcat gcctacgtct ccatccacca tccccatgac 1200
cgactgatgt tcccacggat gctaatgaaa ctggtgagcc tccggaccct gagcagcgtc 1260
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<210> 2
<211> 447
<212> PRT
<213> Homo sapien

<400> 2
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Ala Val Glu Leu Trp Lys Pro Gly Ala Gln Asp Ala Ser Ser Gln Ala

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Gln Gly Gly Ser Ser Cys Ile Leu Arg Glu Glu Ala Arg Met Pro His
          35                        40                        45
Ser Ala Gly Gly Thr Ala Gly Val Gly Leu Glu Ala Ala Glu Pro Thr
          50                        55                        60
Ala Leu Leu Thr Arg Ala Glu Pro Pro Ser Glu Pro Thr Glu Ile Arg
65                        70                        75                        80
Pro Gln Lys Arg Lys Lys Gly Pro Ala Pro Lys Met Leu Gly Asn Glu
                  85                        90                        95
Leu Cys Ser Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Asn Val
                  100                       105                       110
Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Ile Lys
          115                       120                       125
Gly Ala His Tyr Ile Cys His Ser Gly Gly His Cys Pro Met Asp Thr
          130                       135                       140
Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Arg Gln
145                       150                       155                       160
Ala Gly Met Arg Glu Glu Cys Val Leu Ser Glu Glu Gln Ile Arg Leu
                  165                       170                       175
Lys Lys Leu Lys Arg Gln Glu Glu Gln Ala His Ala Thr Ser Leu
          180                       185                       190
Pro Pro Arg Arg Ser Ser Pro Pro Gln Ile Leu Pro Gln Leu Ser Pro
          195                       200                       205
Glu Gln Leu Gly Met Ile Glu Lys Leu Val Ala Ala Gln Gln Gln Cys
          210                       215                       220
Asn Arg Arg Ser Phe Ser Asp Arg Leu Arg Val Thr Pro Trp Pro Met
225                       230                       235                       240
Ala Pro Asp Pro His Ser Arg Glu Ala Arg Gln Gln Arg Phe Ala His
                  245                       250                       255
Phe Thr Glu Leu Ala Ile Val Ser Val Gln Glu Ile Val Asp Phe Ala
                  260                       265                       270
Lys Gln Leu Pro Gly Phe Leu Gln Leu Ser Arg Glu Asp Gln Ile Ala
                  275                       280                       285
Leu Leu Lys Thr Ser Ala Ile Glu Val Met Leu Leu Glu Thr Ser Arg
          290                       295                       300
Arg Tyr Asn Pro Gly Ser Glu Ser Ile Thr Phe Leu Lys Asp Phe Ser
305                       310                       315                       320
Tyr Asn Arg Glu Asp Phe Ala Lys Ala Gly Leu Gln Val Glu Phe Ile
                  325                       330                       335
Asn Pro Ile Phe Glu Phe Ser Arg Ala Met Asn Glu Leu Gln Leu Asn
          340                       345                       350
Asp Ala Glu Phe Ala Leu Leu Ile Ala Ile Ser Ile Phe Ser Ala Asp
          355                       360                       365
Arg Pro Asn Val Gln Asp Gln Leu Gln Val Glu Arg Leu Gln His Thr
          370                       375                       380
Tyr Val Glu Ala Leu His Ala Tyr Val Ser Ile His His Pro His Asp
385                       390                       395                       400
Arg Leu Met Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr
                  405                       410                       415
Leu Ser Ser Val His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln Asp
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Lys Lys Leu Pro Pro Leu Leu Ser Glu Ile Trp Asp Val His Glu
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<210> 3
<211> 1383
<212> DNA
<213> Homo sapien

<400> 3

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ggtccggacc ctgatgtccc aggcactgat gaggccagct cagcctgcag cacagactgg 180
gtcatcccag atcccgaaga ggaaccagag cgcaagcgaa agaagggccc agccccgaag 240
atgctgggcc acgagctttg ccgtgtctgt ggggacaagg cctccggctt ccactacaac 300
gtgctcagct gcgaaggctg caagggcttc ttccggcgca gtgtggtccg tggtggggcc 360
aggcgctatg cctgccgggg tggcggaacc tgccagatgg acgctttcat gcggcgcaag 420
tgccagcagt gccggctgcg caagtgcaag gaggcaggga tgagggagca gtgcgtcctt 480
tctgaagaac agatccggaa gaagaagatt cggaaacagc agcaggagtc acagtcacag 540
tcgcagtcac ctgtggggcc gcagggcagc agcagctcag cctctgggcc tggggcttcc 600
cctggtggat ctgaggcagg cagccagggc tccgggggaag gcgagggtgt ccagctaaca 660
gcggctcaag aactaatgat ccagcagttg gtggcggccc aactgcagtg caacaaacgc 720
tccttctccg accagcccaa agtcacgccc tggcccctgg gcgcagaccc ccagtcccga 780
gatgcccgcc agcaacgctt tgcccacttc acggagctgg ccatcatctc agtccaggag 840
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gccctcctga aggcatccac tatcgagatc atgctgctag agacagccag cgcctacaac 960
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cggctgggcc tggacgacgc tgagtacgcc ctgctcatcg ccatcaacat cttctcggcc 1140
gaccggccca acgtgcagga gccgggccgc gtggaggcgt tgcagcagcc ctacgtggag 1200
gcgctgctgt cctacacgcg catcaagagg ccgcaggacc agctgcgctt cccgcgcatg 1260
ctcatgaagc tggtgagcct gcgcacgctg agctctgtgc actcggagca ggtcttcgcc 1320
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tga                                                                1383

<210> 4
<211> 460
<212> PRT
<213> Homo sapien

<400> 4
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                20                  25                  30
Glu Gly Pro Glu Pro Trp Pro Gly Gly Pro Asp Pro Asp Val Pro Gly
                35                  40                  45
Thr Asp Glu Ala Ser Ser Ala Cys Ser Thr Asp Trp Val Ile Pro Asp
    50                  55                  60
Pro Glu Glu Glu Pro Glu Arg Lys Arg Lys Lys Gly Pro Ala Pro Lys
65                  70                  75                  80
Met Leu Gly His Glu Leu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly
                85                  90                  95
Phe His Tyr Asn Val Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg
                100                 105                 110
Arg Ser Val Val Arg Gly Gly Ala Arg Arg Tyr Ala Cys Arg Gly Gly
            115                 120                 125
Gly Thr Cys Gln Met Asp Ala Phe Met Arg Arg Lys Cys Gln Gln Cys
    130                 135                 140
Arg Leu Arg Lys Cys Lys Glu Ala Gly Met Arg Glu Gln Cys Val Leu
145                 150                 155                 160
Ser Glu Glu Gln Ile Arg Lys Lys Lys Ile Arg Lys Gln Gln Gln Glu
                165                 170                 175
Ser Gln Ser Gln Ser Gln Ser Pro Val Gly Pro Gln Gly Ser Ser Ser
                180                 185                 190
Ser Ala Ser Gly Pro Gly Ala Ser Pro Gly Gly Ser Glu Ala Gly Ser
            195                 200                 205
Gln Gly Ser Gly Glu Gly Glu Gly Val Gln Leu Thr Ala Ala Gln Glu
    210                 215                 220
Leu Met Ile Gln Gln Leu Val Ala Ala Gln Leu Gln Cys Asn Lys Arg
225                 230                 235                 240
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Ser Phe Ser Asp Gln Pro Lys Val Thr Pro Trp Pro Leu Gly Ala Asp
                245                 250                 255
Pro Gln Ser Arg Asp Ala Arg Gln Gln Arg Phe Ala His Phe Thr Glu
                260             265                 270
Leu Ala Ile Ile Ser Val Gln Glu Ile Val Asp Phe Ala Lys Gln Val
            275             280                 285
Pro Gly Phe Leu Gln Leu Gly Arg Glu Asp Gln Ile Ala Leu Leu Lys
        290             295             300
Ala Ser Thr Ile Glu Ile Met Leu Leu Glu Thr Ala Arg Arg Tyr Asn
305             310             315                 320
His Glu Thr Glu Cys Ile Thr Phe Leu Lys Asp Phe Thr Tyr Ser Lys
                325             330                 335
Asp Asp Phe His Arg Ala Gly Leu Gln Val Glu Phe Ile Asn Pro Ile
            340             345             350
Phe Glu Phe Ser Arg Ala Met Arg Arg Leu Gly Leu Asp Asp Ala Glu
        355             360             365
Tyr Ala Leu Leu Ile Ala Ile Asn Ile Phe Ser Ala Asp Arg Pro Asn
    370             375             380
Val Gln Glu Pro Gly Arg Val Glu Ala Leu Gln Gln Pro Tyr Val Glu
385             390             395                 400
Ala Leu Leu Ser Tyr Thr Arg Ile Lys Arg Pro Gln Asp Gln Leu Arg
            405             410                 415
Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser Ser
            420             425                 430
Val His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln Asp Lys Lys Leu
        435             440             445
Pro Pro Leu Leu Ser Glu Ile Trp Asp Val His Glu
    450             455             460
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